

p#15

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## RAW SEQUENCE LISTING

DATE: 05/02/2002 P.6

PATENT APPLICATION: US/09/509,595B

TIME: 16:37:28

Input Set : A:\pto.vsk.txt

Output Set: N:\CRF3\05022002\I509595B.raw

2 <110> APPLICANT: MAX-PLANCK-GESELLSCHAFT ZUR FORDERUNG DER WISSENSCHAFTEN E.V.  
 3 NATIONAL PUBLIC HEALTH INSTITUTE  
 4 PELTONEN, Leena  
 5 AALTONEN, Johanna  
 6 BJORSES, Petra  
 7 PERHEENTUPA, Jaakko  
 8 PALOTIE, Aarno  
 9 HORELLI-KUITUNEN, Nina  
 10 YASPO, Marie-Laure  
 11 LEHRACH, Hans  
 13 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING A (POLY)PEPTIDE CO-  
 SEGREGATING IN MUTATED  
 14 FORM WITH AUTOIMMUNE POLYENDOCRINOPATHY CANDIDIASIS ECTODERMAL DYSTROPHY  
 15 (APECED)  
 17 <130> FILE REFERENCE: VOSS1130  
 19 <140> CURRENT APPLICATION NUMBER: US 09/509,595B  
 20 <141> CURRENT FILING DATE: 2000-07-05  
 22 <150> PRIOR APPLICATION NUMBER: EP 97117154.1  
 23 <151> PRIOR FILING DATE: 1997-10-02  
 25 <150> PRIOR APPLICATION NUMBER: EP 97117398.4  
 26 <151> PRIOR FILING DATE: 1997-10-08  
 28 <150> PRIOR APPLICATION NUMBER: EP 97119810.6  
 29 <151> PRIOR FILING DATE: 1997-11-12  
 31 <160> NUMBER OF SEQ ID NOS: 30  
 33 <170> SOFTWARE: PatentIn version 3.1  
 35 <210> SEQ ID NO: 1  
 36 <211> LENGTH: 2245  
 37 <212> TYPE: DNA  
 38 <213> ORGANISM: Homo sapiens  
 40 <220> FEATURE:  
 41 <221> NAME/KEY: CDS  
 42 <222> LOCATION: (121)..(1758)  
 43 <223> OTHER INFORMATION:  
 45 <400> SEQUENCE: 1  
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 48 gctgccagtgt tcccgggacc caccgcgtcc gccccagccc cgggtccccg cgccccacccc 120  
 50 atg gcg acg gac gcg gcg cta cgc cgg ctt ctg agg ctg cac cgc acg 168  
 51 Met Ala Thr Asp Ala Ala Leu Arg Arg Leu Leu Arg Leu His Arg Thr  
 52 1 5 10 15  
 54 gag atc gcg gtg gcc gtg gac agc gcc ttc cca ctg ctg cac gcg ctg 216  
 55 Glu Ile Ala Val Ala Val Asp Ser Ala Phe Pro Leu Leu His Ala Leu  
 56 20 25 30  
 58 gct gac cac gac gtg gtc ccc gag gac aag ttt cag gag acg ctt cat 264  
 59 Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu His

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60	35	40	45	
62	ctg aag gaa aag gag ggc tgc ccc cag gcc ttc cac gcc ctc ctg tcc	312		
63	Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu Ser			
64	50	55	60	
66	tgg ctg ctg acc cag gac tcc aca gcc atc ctg gac ttc tgg agg gtg	360		
67	Trp Leu Leu Thr Gln Asp Ser Thr Ala Ile Leu Asp Phe Trp Arg Val			
68	65	70	75	80
70	ctg ttc aag gac tac aac ctg gag cgc tat ggc cgg ctg cag ccc atc	408		
71	Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Gly Arg Leu Gln Pro Ile			
72	85	90	95	
74	ctg gac agc ttc ccc aaa gat gtg gac ctc agc cag ccc cgg aag ggg	456		
75	Leu Asp Ser Phe Pro Lys Asp Val Asp Leu Ser Gln Pro Arg Lys Gly			
76	100	105	110	
78	agg aag ccc ccg gcc gtc ccc aag gct ttg gta ccg cca ccc aga ctc	504		
79	Arg Lys Pro Pro Ala Val Pro Lys Ala Leu Val Pro Pro Pro Arg Leu			
80	115	120	125	
82	ccc acc aag agg aag gcc tca gaa gag gct cga gct gcc gcg cca gca	552		
83	Pro Thr Lys Arg Lys Ala Ser Glu Glu Ala Arg Ala Ala Ala Pro Ala			
84	130	135	140	
86	gcc ctg act cca agg ggc acc gcc agc cca ggc tct caa ctg aag gcc	600		
87	Ala Leu Thr Pro Arg Gly Thr Ala Ser Pro Gly Ser Gln Leu Lys Ala			
88	145	150	155	160
90	aag ccc ccc aag aag ccg gag agc agc gca gag cag cag cgc ctt cca	648		
91	Lys Pro Pro Lys Lys Pro Glu Ser Ser Ala Glu Gln Gln Arg Leu Pro			
92	165	170	175	
94	ctc ggg aac ggg att cag acc atg tca gct tca gtc cag aga gct gtg	696		
95	Leu Gly Asn Gly Ile Gln Thr Met Ser Ala Ser Val Gln Arg Ala Val			
96	180	185	190	
98	gcc atg tcc tcc ggg gac gtc ccg gga gcc cga ggg gcc gtg gag ggg	744		
99	Ala Met Ser Ser Gly Asp Val Pro Gly Ala Arg Gly Ala Val Glu Gly			
100	195	200	205	
102	atc ctc atc cag cag gtg ttt gag tca ggc ggc tcc aag aag tgc atc	792		
103	Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Gly Ser Lys Lys Cys Ile			
104	210	215	220	
106	cag gtt ggt ggg gag ttc tac act ccc agc aag ttc gaa gac tcc gcc	840		
107	Gln Val Gly Gly Glu Phe Tyr Thr Pro Ser Lys Phe Glu Asp Ser Gly			
108	225	230	235	240
110	agt ggg aag aac aag gcc cgc agc agc agt ggc ccg aag cct ctg gtt	888		
111	Ser Gly Lys Asn Lys Ala Arg Ser Ser Ser Gly Pro Lys Pro Leu Val			
112	245	250	255	
114	cga gcc aag gga gcc cag ggc gct gcc ccc ggt gga ggt gag gct agg	936		
115	Arg Ala Lys Gly Ala Gln Gly Ala Ala Pro Gly Gly Gly Glu Ala Arg			
116	260	265	270	
118	ctg ggc cag cag ggc agc gtt ccc gcc cct ctg gcc ctc ccc agt gac	984		
119	Leu Gly Gln Gln Gly Ser Val Pro Ala Pro Leu Ala Leu Pro Ser Asp			
120	275	280	285	
122	ccc cag ctc cac cag aag aat gag gac gag tgt gcc gtg tgt cgg gac	1032		
123	Pro Gln Leu His Gln Lys Asp Glu Asp Glu Cys Ala Val Cys Arg Asp			
124	290	295	300	

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126	ggc	ggg	gag	ctc	atc	tgc	tgt	gac	ggc	tgc	cct	cgg	gcc	ttc	cac	ctg	1080
127	Gly	Gly	Glu	Leu	Ile	Cys	Cys	Asp	Gly	Cys	Pro	Arg	Ala	Phe	His	Leu	
128	305					310					315					320	
130	gcc	tgc	ctg	tcc	cct	ccg	ctc	cgg	gag	atc	ccc	agt	ggg	acc	tgg	agg	1128
131	Ala	Cys	Leu	Ser	Pro	Pro	Leu	Arg	Glu	Ile	Pro	Ser	Gly	Thr	Trp	Arg	
132					325					330						335	
134	tgc	tcc	agc	tgc	ctg	cag	gca	aca	gtc	cag	gag	gtg	cag	ccc	cgg	gca	1176
135	Cys	Ser	Ser	Cys	Leu	Gln	Ala	Thr	Val	Gln	Glu	Val	Gln	Pro	Arg	Ala	
136					340					345						350	
138	gag	gag	ccc	cgg	ccc	cag	gag	cca	ccc	gtg	gag	acc	ccg	ctc	ccc	ccg	1224
139	Glu	Glu	Pro	Arg	Pro	Gln	Glu	Pro	Pro	Val	Glu	Thr	Pro	Leu	Pro	Pro	
140			355					360					365				
142	ggg	ctt	agg	tcg	gcg	gga	gag	gag	gta	aga	ggt	cca	cct	ggg	gaa	ccc	1272
143	Gly	Leu	Arg	Ser	Ala	Gly	Glu	Glu	Val	Arg	Gly	Pro	Pro	Gly	Glu	Pro	
144		370					375					380					
146	cta	gcc	ggc	atg	gac	acg	act	ctt	gtc	tac	aag	cac	ctg	ccg	gct	ccg	1320
147	Leu	Ala	Gly	Met	Asp	Thr	Thr	Leu	Val	Tyr	Lys	His	Leu	Pro	Ala	Pro	
148	385					390					395					400	
150	cct	tct	gca	gcc	ccg	ctg	cca	ggg	ctg	gac	tcc	tcg	gcc	ctg	cac	ccc	1368
151	Pro	Ser	Ala	Ala	Pro	Leu	Pro	Gly	Leu	Asp	Ser	Ser	Ala	Leu	His	Pro	
152					405					410						415	
154	cta	ctg	tgt	gtg	ggt	cct	gag	ggt	cag	cag	aac	ctg	gct	cct	ggt	gcg	1416
155	Leu	Leu	Cys	Val	Gly	Pro	Glu	Gly	Gln	Asn	Leu	Ala	Pro	Gly	Ala		
156				420					425					430			
158	cgt	tgc	ggg	gtg	tgc	gga	gat	ggt	acg	gac	gtg	ctg	cgg	tgt	act	cac	1464
159	Arg	Cys	Gly	Val	Cys	Gly	Asp	Gly	Thr	Asp	Val	Leu	Arg	Cys	Thr	His	
160			435					440						445			
162	tgc	gcc	gct	gcc	ttc	cac	tgg	cgc	tgc	cac	ttc	cca	gcc	ggc	acc	tcc	1512
163	Cys	Ala	Ala	Ala	Phe	His	Trp	Arg	Cys	His	Phe	Pro	Ala	Gly	Thr	Ser	
164		450					455					460					
166	cgg	ccc	ggg	acg	ggc	ctg	cgc	tgc	aga	tcc	tgc	tca	gga	gac	gtg	acc	1560
167	Arg	Pro	Gly	Thr	Gly	Leu	Arg	Cys	Arg	Ser	Cys	Ser	Gly	Asp	Val	Thr	
168	465					470					475					480	
170	cca	gcc	cct	gtg	gag	ggg	gtg	ctg	gcc	ccc	agc	ccc	gcc	cgc	ctg	gcc	1608
171	Pro	Ala	Pro	Val	Glu	Gly	Val	Leu	Ala	Pro	Ser	Pro	Ala	Arg	Leu	Ala	
172					485					490						495	
174	cct	ggg	cct	gcc	aag	gat	gac	act	gcc	agt	cac	gag	ccc	gct	ctg	cac	1656
175	Pro	Gly	Pro	Ala	Lys	Asp	Asp	Thr	Ala	Ser	His	Glu	Pro	Ala	Leu	His	
176				500						505						510	
178	agg	gat	gac	ctg	gag	tcc	ctt	ctg	agc	gag	cac	acc	ttc	gat	ggc	atc	1704
179	Arg	Asp	Asp	Leu	Glu	Ser	Leu	Leu	Ser	Glu	His	Thr	Phe	Asp	Gly	Ile	
180			515					520						525			
182	ctg	cag	tgg	gcc	atc	cag	agc	atg	gcc	cgt	ccg	gcg	gcc	ccc	ttc	ccc	1752
183	Leu	Gln	Trp	Ala	Ile	Gln	Ser	Met	Ala	Arg	Pro	Ala	Ala	Pro	Phe	Pro	
184		530					535							540			
186	tcc	tga	ccccagatgg	ccgggacatg	cagctctgat	gagagagtgc	tgagaaggac										1808
187	Ser																
188	545																
190	acctccttcc	tcagtctctgg	aagccggccg	gctgggatca	agaaggggac	agcgccacct											1868

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192 cttgtcagtg ctcggctgta aacagctctg tgtttctggg gacaccagcc atcatgtgcc 1928
194 tggaaattaa accctgcccc acttctctac tctggaagtc cccgggagcc tctccttgcc 1988
196 tggtgaccta ctaaaaatat aaaaattagc tgggtgtggt ggtgggtgcc tgtaatccca 2048
198 gctacatggg agcctgaggc atgagaatca cttgaactcg ggaggtggag gttgcagtga 2108
200 gctgagattg cgccactgca ctccagtctg gtcggcaaga gtgagactcc gtctcaaaaa 2168
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204 attcacatct catgtaa 2245
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208 <211> LENGTH: 545
209 <212> TYPE: PRT
210 <213> ORGANISM: Homo sapiens
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215 1 5 10 15
218 Glu Ile Ala Val Ala Val Asp Ser Ala Phe Pro Leu Leu His Ala Leu
219 20 25 30
222 Ala Asp His Asp Val Val Pro Glu Asp Lys Phe Gln Glu Thr Leu His
223 35 40 45
226 Leu Lys Glu Lys Glu Gly Cys Pro Gln Ala Phe His Ala Leu Leu Ser
227 50 55 60
230 Trp Leu Leu Thr Gln Asp Ser Thr Ala Ile Leu Asp Phe Trp Arg Val
231 65 70 75 80
234 Leu Phe Lys Asp Tyr Asn Leu Glu Arg Tyr Gly Arg Leu Gln Pro Ile
235 85 90 95
238 Leu Asp Ser Phe Pro Lys Asp Val Asp Leu Ser Gln Pro Arg Lys Gly
239 100 105 110
242 Arg Lys Pro Pro Ala Val Pro Lys Ala Leu Val Pro Pro Pro Arg Leu
243 115 120 125
246 Pro Thr Lys Arg Lys Ala Ser Glu Glu Ala Arg Ala Ala Ala Pro Ala
247 130 135 140
250 Ala Leu Thr Pro Arg Gly Thr Ala Ser Pro Gly Ser Gln Leu Lys Ala
251 145 150 155 160
254 Lys Pro Pro Lys Lys Pro Glu Ser Ser Ala Glu Gln Gln Arg Leu Pro
255 165 170 175
258 Leu Gly Asn Gly Ile Gln Thr Met Ser Ala Ser Val Gln Arg Ala Val
259 180 185 190
262 Ala Met Ser Ser Gly Asp Val Pro Gly Ala Arg Gly Ala Val Glu Gly
263 195 200 205
266 Ile Leu Ile Gln Gln Val Phe Glu Ser Gly Gly Ser Lys Lys Cys Ile
267 210 215 220
270 Gln Val Gly Gly Glu Phe Tyr Thr Pro Ser Lys Phe Glu Asp Ser Gly
271 225 230 235 240
274 Ser Gly Lys Asn Lys Ala Arg Ser Ser Ser Gly Pro Lys Pro Leu Val
275 245 250 255
278 Arg Ala Lys Gly Ala Gln Gly Ala Ala Pro Gly Gly Gly Glu Ala Arg
279 260 265 270
282 Leu Gly Gln Gln Gly Ser Val Pro Ala Pro Leu Ala Leu Pro Ser Asp
283 275 280 285
286 Pro Gln Leu His Gln Lys Asn Glu Asp Glu Cys Ala Val Cys Arg Asp

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287      290      295      300
290 Gly Gly Glu Leu Ile Cys Cys Asp Gly Cys Pro Arg Ala Phe His Leu
291 305      310      315      320
294 Ala Cys Leu Ser Pro Pro Leu Arg Glu Ile Pro Ser Gly Thr Trp Arg
295      325      330      335
298 Cys Ser Ser Cys Leu Gln Ala Thr Val Gln Glu Val Gln Pro Arg Ala
299      340      345      350
302 Glu Glu Pro Arg Pro Gln Glu Pro Pro Val Glu Thr Pro Leu Pro Pro
303      355      360      365
306 Gly Leu Arg Ser Ala Gly Glu Glu Val Arg Gly Pro Pro Gly Glu Pro
307      370      375      380
310 Leu Ala Gly Met Asp Thr Thr Leu Val Tyr Lys His Leu Pro Ala Pro
311 385      390      395      400
314 Pro Ser Ala Ala Pro Leu Pro Gly Leu Asp Ser Ser Ala Leu His Pro
315      405      410      415
318 Leu Leu Cys Val Gly Pro Glu Gly Gln Gln Asn Leu Ala Pro Gly Ala
319      420      425      430
322 Arg Cys Gly Val Cys Gly Asp Gly Thr Asp Val Leu Arg Cys Thr His
323      435      440      445
326 Cys Ala Ala Ala Phe His Trp Arg Cys His Phe Pro Ala Gly Thr Ser
327      450      455      460
330 Arg Pro Gly Thr Gly Leu Arg Cys Arg Ser Cys Ser Gly Asp Val Thr
331 465      470      475      480
334 Pro Ala Pro Val Glu Gly Val Leu Ala Pro Ser Pro Ala Arg Leu Ala
335      485      490      495
338 Pro Gly Pro Ala Lys Asp Asp Thr Ala Ser His Glu Pro Ala Leu His
339      500      505      510
342 Arg Asp Asp Leu Glu Ser Leu Leu Ser Glu His Thr Phe Asp Gly Ile
343      515      520      525
346 Leu Gln Trp Ala Ile Gln Ser Met Ala Arg Pro Ala Ala Pro Phe Pro
347      530      535      540
350 Ser
351 545
354 <210> SEQ ID NO: 3
355 <211> LENGTH: 90
356 <212> TYPE: DNA
357 <213> ORGANISM: Murine
359 <400> SEQUENCE: 3
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362 ttctgttgat ctccagtcag aggctggggg 90
365 <210> SEQ ID NO: 4
366 <211> LENGTH: 90
367 <212> TYPE: DNA
368 <213> ORGANISM: Homo sapiens
370 <400> SEQUENCE: 4
371 aaggggctgg tgtggaaagc cccacggcat ggtggaaagt ccgaaattct acaggggcct 60
373 ctttgttaaa cctccatgca agaggctggg 90
376 <210> SEQ ID NO: 5
377 <211> LENGTH: 90

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/509,595B

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Input Set : A:\pto.vsk.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 1,2,4,7,8,9,12,13,14,16,19,24,25,26,28,29,32,43,56,58,61,63  
Seq#:5; N Pos. 68,70,72,73,75,76,78,79,80,83,84,85,86,87  
Seq#:10; Xaa Pos. 1,2,3,5,6,22,48,69,72,80,91,94,95,99,107,109,116,118,122  
Seq#:10; Xaa Pos. 124,128,135,138,141,142,145,147,148,149,150,151,152,157  
Seq#:10; Xaa Pos. 160,167,168,169,170,172,174,185,193,194,195,202,219,234  
Seq#:10; Xaa Pos. 239,242,243,250,252,253,256,264,265,266,269,270,272,273  
Seq#:10; Xaa Pos. 274,278,279,282,283,284,285,289,292,293,304,329,335,340  
Seq#:10; Xaa Pos. 344,345,348,349,350,351,352,353,355,356,359,361,363,367  
Seq#:10; Xaa Pos. 368,369,375,377,378,382,383,385,386,388,389,391,392,393  
Seq#:10; Xaa Pos. 394,396,397,399,402,403,408,409,411,412,416,420,421,423  
Seq#:10; Xaa Pos. 426,427,428,429,432,436,443,448,462,463,464,465,470,474  
Seq#:10; Xaa Pos. 478,480,483,485,486,487,489,490,491,493,495,496,498,502  
Seq#:10; Xaa Pos. 505,506,509,513,515,526,529,542,545,547,548,550  
Seq#:30; Xaa Pos. 2,3,5,6,7,8,9,10,11,12,14,15,17,18,19,20,22,23,25,26,27  
Seq#:30; Xaa Pos. 28,29,30,31,32,33,34,35,36,37,38,40,41

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 13

## VERIFICATION SUMMARY

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L:390 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0  
L:392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:60  
L:1003 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0  
L:1007 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:16  
L:1011 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:32  
L:1019 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:64  
L:1023 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:80  
L:1027 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:96  
L:1031 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:112  
L:1035 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:128  
L:1039 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:144  
L:1043 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:160  
L:1047 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:176  
L:1051 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:192  
L:1055 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:208  
L:1059 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:224  
L:1063 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:240  
L:1067 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:256  
L:1071 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:272  
L:1075 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:288  
L:1083 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:320  
L:1087 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:336  
L:1091 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:352  
L:1095 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:368  
L:1099 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:384  
L:1103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:400  
L:1107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:416  
L:1111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:432  
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L:1119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:464  
L:1123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:480  
L:1127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:496  
L:1131 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:512  
L:1135 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:528  
L:1139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:544  
L:1380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0  
L:1384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:16  
L:1388 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:32